REMARKS

The Office Action rejected claims 39-58 under 35 U.S.C. §112, 2nd paragraph and under 35 U.S.C. § 101 as claiming the same invention as that of claims 1-8, 11-15, and 18-24 of U.S. Patent No. 6,361,947 B1.

Rejection under 35 USC §112, second paragraph

Claim 39 has been amended to clarify that the fragments being amplified are the fragments to which an adaptor sequence has been ligated. Applicants thank the Examiner for the helpful suggestion for a clarifying amendment and have incorporated the Examiner's suggested amendment.

Rejection under 35 USC §101

The test for statutory double patenting requires that claims from the application at issue and a patent must define exactly the same scope. If there is an embodiment that falls within the scope of one claim, but not the other, then the claim scope is not identical and statutory double patenting does not exist. The MPEP gives the example of a claim to a compound having a "halogen" substituent and a claim reciting the same compound except having a "chlorine" substituent in place of the halogen. Halogen is not identical to chlorine, but is broader than chlorine so the claims are not identical or substantively the same and should not be subject to a statutory double patenting rejection. MPEP 804(II)(A). Applicants assert that claim 39 of the present application and claim 1 of U.S. Patent No. 6,361,947 are analogous to the halogen and chlorine example. Claim 1 of '947 claims alternative embodiments (a)-(e) while claim 39 of the pending application claims an embodiment analogous to embodiment (a) of claim 1 of '947. Embodiments (b)-(e) fall within the scope of claim 1 of '947 but not within the scope of claim 39 of the pending application. Claims 40-58 are dependent on claim 39. The claims are not

coextensive in scope, therefore, a statutory type double patenting rejection should not apply. Claim 1 of the 6,361,947 patent is reproduced below:

1. A method of analyzing a first nucleic acid sample comprising:

providing said first nucleic acid sample;

obtaining a second nucleic acid sample by:

(a) fragmenting said first nucleic acid sample to produce fragments, ligating adaptor sequences to said fragments, amplifying at least some of said fragments, and isolating said amplified fragments; or

(b) fragmenting said first nucleic acid sample to produce fragments, denaturing said fragments, allowing at least some of said fragments to reanneal to form double stranded DNA sequences and removing said double stranded DNA sequences thus isolating said single stranded fragments; or

(c) amplifying said first nucleic acid sample by arbitrarily primed PCR to produce an amplification product and isolating said amplification product; or

(d) fragmenting said first nucleic acid sample to produce fragments, hybridizing said fragments to an oligonucleotide probe bound to a solid support, and isolating said hybridized fragments; or

(e) fragmenting said first nucleic acid sample to produce fragments, binding said fragments to a mismatch binding protein, and isolating said bound fragments;

providing a nucleic acid array;

hybridizing said second nucleic acid sample to said array; and analyzing a hybridization pattern resulting from said hybridization.

CONCLUSION

For the foregoing reasons, Applicants believe all the pending claims are now in condition for allowance and should be passed to issue. Applicants believe that no extension of time is required for submission of this paper. However, if an extension is required, Applicants petition for any necessary extension of time and authorize the Commissioner to deduct any required fees from the undersigned's Deposit Account No.

01-0431. Please deduct any additional fees from, or credit any overpayment to the above-noted Deposit Account. If the Examiner feels that a telephone conference would in any way expedite the prosecution of the application, please do not hesitate to call the undersigned at (408) 731-5768.

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Respectfully submitted,

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Version with markings to show changes

In the claims

39. A method of analyzing a first nucleic acid sample comprising:

providing said first nucleic acid sample;

obtaining a second nucleic acid sample by fragmenting said first nucleic acid sample to produce fragments, ligating adaptor sequences to said fragments, amplifying at least some of said fragments ligated with said adaptor sequences, and isolating said amplified fragments;

providing a nucleic acid array;

hybridizing said second nucleic acid sample to said array; and

analyzing a hybridization pattern resulting from said hybridization.